

Picard Preprocess-1.98

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Community rating: ?????

Quick Start

- To use **Picard Preprocess**, import your alignment output data in SAM/BAM format.
- *Resources: <http://broadinstitute.github.io/picard/index.html>

Test Data



Test data for this app appears directly in the Discovery Environment in the Data window under *Shared With Me* -> *luj* -> *variant_calling*.

Input File(s)

Use directory **bwa_output** from the directory above as test input directory containing alignment output.

Parameters Used in App

When the app is run in the Discovery Environment, use the following parameters with the above input directory to get the output provided in the next section below.

- Default parameters only, no further configuration needed.

Advanced Use

The app will extract read group info from the file names if you following assumed naming convention as following:

ex. CAAS_B093_120319_I631_FCC0J86ACXX_L4_RICxaoRSYHSD8-4-IPAAPEKF-62.sam

the read group id is 120319_I631_FCC0J86ACXX_L4

the read group sample name is CAAS_B093

the read group platform unit is 120319_I631

the read group platform is Illumina which is default

the read group library is RICxaoRSYHSD8-4-IPAAPEKF-62

All except read group platform will be extracted from file name if you leave the read group info field empty in Parameters panel. If your file naming convention is different, you have to enter one bam file as input a time and enter the read group information in the Parameters panel.

Output File(s)

Expect a directory file named **picard_preprocess_output** as output directory containing processed alignment outputs.

Tool Source for App

- <http://broadinstitute.github.io/picard/index.html>